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SEQUENCE LISTING

<110> Kato, Seishi
 Sekine, Shingo
 Kimura, Tomoko
 Nakamura, Nobuko

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND CDNAS
 ENCODING THESE PROTEINS

<130> GIN-6714CPUS

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<150> JP 10-046607

<151> 1998-02-27

<150> PCT/JP99/00875

<151> 1999-02-25

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<212> PRT

<213> Homo sapiens

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 20 25 30

Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys Thr Ser Lys Lys
 35 40 45

Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu Ala Lys Asp Gly
 50 55 60

Ser Lys Phe Tyr Cys Ser Arg Thr Gln Asn Glu Gly His Pro Lys Trp
 65 70 75 80

Phe Val Leu Gly Val Gly Gln Val Ile Lys Gly Leu Asp Ile Ala Met
 85 90 95

Thr Asp Met Cys Pro Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser
 100 105 110

Phe Ala Tyr Gly Lys Glu Gly Tyr Asp Lys Pro Leu Leu Ala Lys Gly
 115 120 125

Ile

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Tyr Leu Lys Arg Leu Pro Val Pro Glu Ser Ile Thr Gly Phe Ala Arg
20 25 30

Leu Thr Val Ser Glu Trp Leu Arg Leu Leu Pro Phe Leu Gly Val Leu
35 40 45

Ala Leu Leu Gly Tyr Leu Ala Val Arg Pro Phe Leu Pro Lys Lys Lys
50 55 60

Gln Gln Lys Asp Ser Leu Ile Asn Leu Lys Ile Gln Lys Glu Asn Pro
65 70 75 80

Lys Val Val Asn Glu Ile Asn Ile Glu Asp Leu Cys Leu Thr Lys Ala
85 90 95

Ala Tyr Cys Arg Cys Trp Arg Ser Lys Thr Phe Pro Ala Cys Asp Gly
100 105 110

Ser His Asn Lys His Asn Glu Leu Thr Gly Asp Asn Val Gly Pro Leu
115 120 125

Ile Leu Lys Lys Lys Glu Val
130 135

<210> 3

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<213> Homo sapiens

<400> 3

Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe
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Asp Arg Val Lys Met Gly Phe Val Met Gly Cys Ala Val Gly Met Ala
20 25 30

Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu Arg Ile Gly Met Arg
35 40 45

Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr Met Met Gln Ser Gly
50 55 60

Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met Gly Ile Arg Cys
65 70 75

<210> 4

<211> 144

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu Leu
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Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
20 25 30

Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Thr Leu
35 40 45

Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala Phe Phe Cys Val
50 55 60

Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu Gly Leu Asn Met Pro
65 70 75 80

Leu Leu Ala Tyr His Ile Trp Arg Tyr Met Ser Arg Pro Val Met Ser
85 90 95

Gly Pro Gly Leu Tyr Asp Pro Thr Thr Ile Met Asn Ala Asp Ile Leu
100 105 110

Ala Tyr Cys Gln Lys Glu Gly Trp Cys Lys Leu Ala Phe Tyr Leu Leu
115 120 125

Ala Phe Phe Tyr Tyr Leu Tyr Gly Met Ile Tyr Val Leu Val Ser Ser
130 135 140

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<213> Homo sapiens

<400> 5

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20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
85 90 95

Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser

115

120

125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
260 265 270

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<210> 6

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<400> 6

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20 25 30

Phe Met Tyr Ala Lys Arg Asn Lys Arg Arg Ile Met Arg Ile Phe Ser
35 40 45

Val Pro Pro Thr Glu Glu Thr Leu Ser Glu Pro Asn Phe Tyr Asp Thr
50 55 60

Ile Ser Lys Ile Arg Leu Arg Gln Gln Leu Glu Met Tyr Ser Ile Ser
65 70 75 80

Arg Lys Tyr Asp Tyr Gln Gln Pro Gln Asn Gln Ala Asp Ser Val Gln
85 90 95

Leu Ser Leu Glu

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<210> 7
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<212> PRT
<213> Homo sapiens

<400> 7

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Thr His Ile Asp Val His Ile His Gln Glu Ser Ala Leu Ala Lys Leu
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Leu Leu Thr Cys Cys Ser Ala Leu Arg Pro Arg Ala Thr Gln Ala Arg
35 40 45
Gly Ser Ser Arg Leu Leu Val Ala Ser Trp Val Met Gln Ile Val Leu
50 55 60
Gly Ile Leu Ser Ala Val Leu Gly Gly Phe Phe Tyr Ile Arg Asp Tyr
65 70 75 80
Thr Leu Leu Val Thr Ser Gly Ala Ala Ile Trp Thr Gly Ala Val Ala
85 90 95
Val Leu Ala Gly Ala Ala Ala Phe Ile Tyr Glu Lys Arg Gly Gly Thr
100 105 110
Tyr Trp Ala Leu Leu Arg Thr Leu Leu Ala Leu Ala Ala Phe Ser Thr
115 120 125
Ala Ile Ala Ala Leu Lys Leu Trp Asn Glu Asp Phe Arg Tyr Gly Tyr
130 135 140
Ser Tyr Tyr Asn Ser Ala Cys Arg Ile Ser Ser Ser Ser Asp Trp Asn
145 150 155 160
Thr Pro Ala Pro Thr Gln Ser Pro Glu Glu Val Arg Arg Leu His Leu
165 170 175
Cys Thr Ser Phe Met Asp Met Leu Lys Ala Leu Phe Arg Thr Leu Gln
180 185 190
Ala Met Leu Leu Gly Val Trp Ile Leu Leu Leu Leu Ala Ser Leu Ala
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Pro Leu Trp Leu Tyr Cys Trp Arg Met Phe Pro Thr Lys Gly Val Ser
210 215 220

Pro
225

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<212> DNA
<213> Homo sapiens

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aactgctcta agacaagcaa gaagggagac ctactaaatg cccattatga cggctacctg 180
gctaaagacg gctcgaaatt ctactgcagc cggacacaaa atgaaggcca ccccaaattg 240
tttgttcttg gtgttgggca agtcataaaa ggcctagaca ttgctatgac agatatgtgc 300
cctggagaaa agcgaaaagt agttataccc ccttcatttg catacggaag ggaaggctat 360
gataaacctc tacttgcaaa gggaatt 387

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<212> DNA
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ttattgcctt tccttgggtg actcgcactt ctgggtacc ttgcagttcg tccattcctc 180
ccgaagaaga aacaacagaa ggatagcttg attaacttta aaatacaaaa ggaaaatccg 240
aaagtagtga atgaaataaa cattgaagat ttgtgtctta ctaaagcagc ttattgtagg 300
tggtggcgtt ctaaaacgtt tcctgcctgc gatgggtcac ataataaaca caatgaattg 360
acaggagata atgtgggtcc actaatactg aagaagaaag aagta 405

<210> 10
<211> 237
<212> DNA
<213> Homo sapiens

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tcctgtctca ggatcggaat gcggggtcga gagctgatgg gcggcatttg gaaaaccatg 180
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<210> 11
<211> 432
<212> DNA
<213> Homo sapiens

<400> 11
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cctatagacc agtgtaatac cctgaatccc ctgtactcc cagagtacct catccacgt 180
ttcttctgtg tcatgtttct ttgtgcagca gagtggctta cactgggtct caatatgcc 240
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tatgacccta caaccatcat gaatgcagat attctagcat attgtcagaa ggaaggatgg 360
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ttggtgagct ct 432

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<211> 846
<212> DNA
<213> Homo sapiens

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ccgacctctg	cccaggccgc	aggccccagc	tcaggctcgt	gcccacccac	caagttccag	180
tgccgcacca	gtggcttatg	cgtgccccctc	acctggcgct	gcgacagga	cttggactgc	240
agcgatggca	gcgatgagga	ggagtgcagg	attgagccat	gtaccagaa	agggcaatgc	300
ccaccgcccc	ctggcctccc	ctgcccctgc	accggcgtea	gtgactgctc	tgggggaact	360
gacaagaaac	tgcgcaactg	cagccgcctg	gcctgcctag	caggcgagct	ccgttgacag	420
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tccagcgacg	agctcggctg	tggaaaccaat	gagatcctcc	cggaagggga	tgccacaacc	540
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ccccctgtga	ccctggagag	tgtcccctct	gtcgggaatg	ccacatcctc	ctctgccgga	660
gaccagtctg	gaagcccaac	tgcctatggg	gttattgcag	ctgctgcggt	gctcagtgc	720
agcctgggtc	ccgccaccct	cctccttttg	tcctggctcc	gagcccagga	gcgcctccgc	780
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ctgccc						846

<210> 13
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 <212> DNA
 <213> Homo sapiens

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gtttacttga	tagttatcct	tgtagcttc	ggtctcttca	tgtatgccaa	aaggaacaaa	120
aggagaatta	tgaggatatt	cagtgtgcca	cctacagagg	aaactttgtc	agagcccaac	180
ttttatgaca	cgataagcaa	gattcgttta	agacaacaac	tggaaatgta	ttccatttca	240
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 <212> DNA
 <213> Homo sapiens

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cagatcgtgc	tggggatcct	gagtgcagtc	ctaggaggat	ttttctacat	ccgcgactac	240
accctcctcg	tcacctcggg	agctgccatc	tggacagggg	ctgtggctgt	gctggctgga	300
gctgctgcct	tcatttacga	gaaacggggg	ggtacatact	gggccctgct	gaggactctg	360
ctagcgctgg	cagctttctc	cacagccatc	gctgcctca	aactttggaa	tgaagatttc	420
cgatatggct	actcttatta	caacagtgcc	tgccgcatct	ccagctcgag	tgactggaac	480
actccagccc	ccactcagag	tccagaagaa	gtcagaaggc	tacacctatg	tacctccttc	540
atggacatgc	tgaaggcctt	gttcagaacc	cttcaggcca	tgctcttggg	tgtctggatt	600
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (70) .. (456)

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ccaaaaaacc atg cat ttc tta ttc aga ttc att gtt ttc ttt tat ctg tgg 111
 Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr Leu Trp
 1 5 10

ggc ctt ttt act gct cag aga caa aag aaa gag gag agc acc gaa gaa 159
 Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr Glu Glu
 15 20 25 30

gtg aaa ata gaa gtt ttg cat cgt cca gaa aac tgc tct aag aca agc 207
 Val Lys Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys Thr Ser
 35 40 45

aag aag gga gac cta cta aat gcc cat tat gac ggc tac ctg gct aaa 255
 Lys Lys Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu Ala Lys
 50 55 60

gac ggc tgc aaa ttc tac tgc agc cgg aca caa aat gaa ggc cac ccc 303
 Asp Gly Ser Lys Phe Tyr Cys Ser Arg Thr Gln Asn Glu Gly His Pro
 65 70 75

aaa tgg ttt gtt ctt ggt gtt ggg caa gtc ata aaa ggc cta gac att 351
 Lys Trp Phe Val Leu Gly Val Gly Gln Val Ile Lys Gly Leu Asp Ile
 80 85 90

gct atg aca gat atg tgc cct gga gaa aag cga aaa gta gtt ata ccc 399
 Ala Met Thr Asp Met Cys Pro Gly Glu Lys Arg Lys Val Val Ile Pro
 95 100 105 110

cct tca ttt gca tac gga aag gaa ggc tat gat aaa cct cta ctt gca 447
 Pro Ser Phe Ala Tyr Gly Lys Glu Gly Tyr Asp Lys Pro Leu Leu Ala
 115 120 125

aag gga att tgaaaaagat gagaagccac gtgacaagtc atatcaggat 496
 Lys Gly Ile

gcagtttttag aagatatattt taagaagaat gaccatgatg gtgatggctt cattttctccc 556

aaggaataca atgtatacca acacgatgaa ctatagcata tttgtatttc tactttttttt 616

tttagctatt tactgtactt tatgtataaa acaaagtcac ttttctccaa gttgtatttg 676

ctatttttcc cctatgagaa gatattttga tctccccaat acattgattt tggataata 736

aaatgtgagg ctgttttgca aactt 761

<210> 16

<211> 129

<212> PRT

<213> Homo sapiens

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Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr Glu Glu Val Lys

20

25

30

Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys Thr Ser Lys Lys
 35 40 45

Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu Ala Lys Asp Gly
 50 55 60

Ser Lys Phe Tyr Cys Ser Arg Thr Gln Asn Glu Gly His Pro Lys Trp
 65 70 75 80

Phe Val Leu Gly Val Gly Gln Val Ile Lys Gly Leu Asp Ile Ala Met
 85 90 95

Thr Asp Met Cys Pro Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser
 100 105 110

Phe Ala Tyr Gly Lys Glu Gly Tyr Asp Lys Pro Leu Leu Ala Lys Gly
 115 120 125

Ile

<210> 17

<211> 701

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (46)..(450)

<400> 17

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 Ser Val Ala Arg Ile Val Lys Val Gln Leu Pro Ala Tyr Leu Lys Arg
 5 10 15 20

ctc cca gtc cct gaa agc att acc ggg ttc gct agg ctc aca gtt tca 153
 Leu Pro Val Pro Glu Ser Ile Thr Gly Phe Ala Arg Leu Thr Val Ser
 25 30 35

gaa tgg ctt cgg tta ttg cct ttc ctt ggt gta ctc gca ctt ctt ggc 201
 Glu Trp Leu Arg Leu Leu Pro Phe Leu Gly Val Leu Ala Leu Leu Gly
 40 45 50

tac ctt gca gtt cgt cca ttc ctc ccg aag aag aaa caa cag aag gat 249
 Tyr Leu Ala Val Arg Pro Phe Leu Pro Lys Lys Lys Gln Gln Lys Asp
 55 60 65

agc ttg att aat ctt aaa ata caa aag gaa aat ccg aaa gta gtg aat 297
 Ser Leu Ile Asn Leu Lys Ile Gln Lys Glu Asn Pro Lys Val Val Asn
 70 75 80

gaa ata aac att gaa gat ttg tgt ctt act aaa gca gct tat tgt agg 345
 Glu Ile Asn Ile Glu Asp Leu Cys Leu Thr Lys Ala Ala Tyr Cys Arg
 85 90 95 100

tgt tgg cgt tct aaa acg ttt cct gcc tgc gat ggt tca cat aat aaa 393
 Cys Trp Arg Ser Lys Thr Phe Pro Ala Cys Asp Gly Ser His Asn Lys
 105 110 115

cac aat gaa ttg aca gga gat aat gtg ggt cca cta ata ctg aag aag 441
 His Asn Glu Leu Thr Gly Asp Asn Val Gly Pro Leu Ile Leu Lys Lys
 120 125 130

aaa gaa gta taataataat aacaatattt tctcattctt tgtgtataga 490
 Lys Glu Val
 135

aaattttaaa atgggtggtct taattattac tactgggtga acaattattt cttccaattt 550

attttcttcc tgcactactg tttgtatttg atcctttgtc tattcagtca cttaattaga 610

aattaaattg tcaagcctct tattctgact tcaaagaatt aatgtatctt ccaacaataa 670

aatcacttct gattttaatc taggaaaacc t 701

<210> 18

<211> 135

<212> PRT

<213> Homo sapiens

<400> 18

Met Val Leu Glu Ser Val Ala Arg Ile Val Lys Val Gln Leu Pro Ala
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Tyr Leu Lys Arg Leu Pro Val Pro Glu Ser Ile Thr Gly Phe Ala Arg
 20 25 30

Leu Thr Val Ser Glu Trp Leu Arg Leu Leu Pro Phe Leu Gly Val Leu
 35 40 45

Ala Leu Leu Gly Tyr Leu Ala Val Arg Pro Phe Leu Pro Lys Lys Lys
 50 55 60

Gln Gln Lys Asp Ser Leu Ile Asn Leu Lys Ile Gln Lys Glu Asn Pro
 65 70 75 80

Lys Val Val Asn Glu Ile Asn Ile Glu Asp Leu Cys Leu Thr Lys Ala
 85 90 95

Ala Tyr Cys Arg Cys Trp Arg Ser Lys Thr Phe Pro Ala Cys Asp Gly
 100 105 110

Ser His Asn Lys His Asn Glu Leu Thr Gly Asp Asn Val Gly Pro Leu
 115 120 125

Ile Leu Lys Lys Lys Glu Val

135

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<220>  
<221> CDS  
<222> (81) .. (317)
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<210> 20
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<212> PRT
<213> Homo sapiens
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Asp  Arg  Val  Lys  Met  Gly  Phe  Val  Met  Gly  Cys  Ala  Val  Gly  Met  Ala
              20              25              30
Ala  Gly  Ala  Leu  Phe  Gly  Thr  Phe  Ser  Cys  Leu  Arg  Ile  Gly  Met  Arg
              35              40              45
Gly  Arg  Glu  Leu  Met  Gly  Gly  Ile  Gly  Lys  Thr  Met  Met  Gln  Ser  Gly

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50

55

60

Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met Gly Ile Arg Cys
 65 70 75

<210> 21
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 <212> DNA
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<220>
 <221> CDS
 <222> (48)..(479)

<400> 21

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 Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu Leu Thr Ala Ala
 5 10 15

ctc atc ttc ttc gcc att tgg cac att ata gca ttt gat gag ctg aag 152
 Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp Glu Leu Lys
 20 25 30 35

act gat tac aag aat cct ata gac cag tgt aat acc ctg aat ccc ctt 200
 Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Thr Leu Asn Pro Leu
 40 45 50

gta ctc cca gag tac ctc atc cac gct ttc ttc tgt gtc atg ttt ctt 248
 Val Leu Pro Glu Tyr Leu Ile His Ala Phe Phe Cys Val Met Phe Leu
 55 60 65

tgt gca gca gag tgg ctt aca ctg ggt ctc aat atg ccc ctc ttg gca 296
 Cys Ala Ala Glu Trp Leu Thr Leu Gly Leu Asn Met Pro Leu Leu Ala
 70 75 80

tat cat att tgg agg tat atg agt aga cca gtg atg agt ggc cca gga 344
 Tyr His Ile Trp Arg Tyr Met Ser Arg Pro Val Met Ser Gly Pro Gly
 85 90 95

ctc tat gac cct aca acc atc atg aat gca gat att cta gca tat tgt 392
 Leu Tyr Asp Pro Thr Thr Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys
 100 105 110 115

cag aag gaa gga tgg tgc aaa tta gct ttt tat ctt cta gca ttt ttt 440
 Gln Lys Glu Gly Trp Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe
 120 125 130

tac tac cta tat ggc atg atc tat gtt ttg gtg agc tct tagaacaaca 489
 Tyr Tyr Leu Tyr Gly Met Ile Tyr Val Leu Val Ser Ser
 135 140

cacagaagaa ttggtccagt taagtgcagt caaaaagcca ccaaataag ggattctatc 549

cagcaagatc ctgtccaaga gtagcctgtg gaatctgatc agttacttta aaaaatgact 609
 ccttattttt taaatgtttc cacatttttg cttgtggaaa gactgttttc atatgttata 669
 ctcagataaa gatttttaaat ggtattacgt ataaattaat ataaaatgat tacctctggg 729
 gttgacaggt ttgaacttgc acttccttaag gaacagccat aatcctctga atgatgcatt 789
 aattactgac tgtcctagta cattggaagc ttttgtttat aggaacttgt agggctcatt 849
 ttggtttcat tgaaacagta tctaattata aattagctgt agatatcagg tgcttctgat 909
 gaagtgaaaa tgtatatctg actagtggga aacttcatgg gtttctcat ctgtcatgtc 969
 gatgattata tatggatata tttaaaaaa taaaagcgg gaattttccc ttcgcttgaa 1029
 tatt 1033

<210> 22
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 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu Leu
 1 5 10 15
 Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
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 Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Thr Leu
 35 40 45
 Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala Phe Phe Cys Val
 50 55 60
 Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu Gly Leu Asn Met Pro
 65 70 75 80
 Leu Leu Ala Tyr His Ile Trp Arg Tyr Met Ser Arg Pro Val Met Ser
 85 90 95
 Gly Pro Gly Leu Tyr Asp Pro Thr Thr Ile Met Asn Ala Asp Ile Leu
 100 105 110
 Ala Tyr Cys Gln Lys Glu Gly Trp Cys Lys Leu Ala Phe Tyr Leu Leu
 115 120 125
 Ala Phe Phe Tyr Tyr Leu Tyr Gly Met Ile Tyr Val Leu Val Ser Ser
 130 135 140

<210> 23
 <211> 1270
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86)..(931)

<400> 23

ccccgcccc accccgcgcg tgcgcgtgcg cagggataag agagcgggtct ggacagcgcg 60

tggccggcgc cgctgtgggg acagc atg agc ggc ggt tgg atg gcg cag gtt 112
Met Ser Gly Gly Trp Met Ala Gln Val
1 5

gga gcg tgg cga aca ggg gct ctg ggc ctg gcg ctg ctg ctg ctg ctc 160
Gly Ala Trp Arg Thr Gly Ala Leu Gly Leu Ala Leu Leu Leu Leu Leu
10 15 20 25

ggc ctc gga cta ggc ctg gag gcc gcc gcg agc ccg ctt tcc acc ccg 208
Gly Leu Gly Leu Gly Leu Glu Ala Ala Ser Pro Leu Ser Thr Pro
30 35 40

acc tct gcc cag gcc gca ggc ccc agc tca ggc tgc tgc cca ccc acc 256
Thr Ser Ala Gln Ala Ala Gly Pro Ser Ser Gly Ser Cys Pro Pro Thr
45 50 55

aag ttc cag tgc cgc acc agt ggc tta tgc gtg ccc ctc acc tgg cgc 304
Lys Phe Gln Cys Arg Thr Ser Gly Leu Cys Val Pro Leu Thr Trp Arg
60 65 70

tgc gac agg gac ttg gac tgc agc gat ggc agc gat gag gag gag tgc 352
Cys Asp Arg Asp Leu Asp Cys Ser Asp Gly Ser Asp Glu Glu Glu Cys
75 80 85

agg att gag cca tgt acc cag aaa ggg caa tgc cca ccg ccc cct ggc 400
Arg Ile Glu Pro Cys Thr Gln Lys Gly Gln Cys Pro Pro Pro Pro Gly
90 95 100 105

ctc ccc tgc ccc tgc acc ggc gtc agt gac tgc tct ggg gga act gac 448
Leu Pro Cys Pro Cys Thr Gly Val Ser Asp Cys Ser Gly Gly Thr Asp
110 115 120

aag aaa ctg cgc aac tgc agc cgc ctg gcc tgc cta gca ggc gag ctc 496
Lys Lys Leu Arg Asn Cys Ser Arg Leu Ala Cys Leu Ala Gly Glu Leu
125 130 135

cgt tgc acg ctg agc gat gac tgc att cca ctc acg tgg cgc tgc gac 544
Arg Cys Thr Leu Ser Asp Asp Cys Ile Pro Leu Thr Trp Arg Cys Asp
140 145 150

ggc cac cca gac tgt ccc gac tcc agc gac gag ctc ggc tgt gga acc 592
Gly His Pro Asp Cys Pro Asp Ser Ser Asp Glu Leu Gly Cys Gly Thr
155 160 165

aat gag atc ctc ccg gaa ggg gat gcc aca acc atg ggg ccc cct gtg 640
Asn Glu Ile Leu Pro Glu Gly Asp Ala Thr Thr Met Gly Pro Pro Val
170 175 180 185

acc ctg gag agt gtc acc tct ctc agg aat gcc aca acc atg ggg ccc 688
 Thr Leu Glu Ser Val Thr Ser Leu Arg Asn Ala Thr Thr Met Gly Pro
 190 195 200

cct gtg acc ctg gag agt gtc ccc tct gtc ggg aat gcc aca tcc tcc 736
 Pro Val Thr Leu Glu Ser Val Pro Ser Val Gly Asn Ala Thr Ser Ser
 205 210 215

tct gcc gga gac cag tct gga agc cca act gcc tat ggg gtt att gca 784
 Ser Ala Gly Asp Gln Ser Gly Ser Pro Thr Ala Tyr Gly Val Ile Ala
 220 225 230

gct gct gcg gtg ctc agt gca agc ctg gtc acc gcc acc ctc ctc ctt 832
 Ala Ala Ala Val Leu Ser Ala Ser Leu Val Thr Ala Thr Leu Leu Leu
 235 240 245

ttg tcc tgg ctc cga gcc cag gag cgc ctc cgc cca ctg ggg tta ctg 880
 Leu Ser Trp Leu Arg Ala Gln Glu Arg Leu Arg Pro Leu Gly Leu Leu
 250 255 260 265

gtg gcc atg aag gag tcc ctg ctg ctg tca gaa cag aag acc tcg ctg 928
 Val Ala Met Lys Glu Ser Leu Leu Leu Ser Glu Gln Lys Thr Ser Leu
 270 275 280

ccc tgaggacaag cacttgccac caccgtcact cagccctggg cgtagccgga 981
 Pro

caggaggaga gcagtgatgc ggatgggtac ccgggcacac cagccctcag agacctgagc 1041

tcttctggcc acgtggaacc tcgaaccga gctcctgcag aagtggccct ggagattgag 1101

ggtccttgga cactccctat ggagatccgg ggagctagga tggggaacct gccacagcca 1161

gaactgaggg gctggcccca ggcagctccc agggggtaga acggccctgt gcttaagaca 1221

ctcctgctgc cccgtctgag ggtggcgatt aaagttgctt cacatcctc 1270

<210> 24

<211> 282

<212> PRT

<213> Homo sapiens

<400> 24

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
 1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
 20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
 35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
 50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys

65		70		75		80
Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln	85		90		95	
Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly	100		105		110	
Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser	115		120		125	
Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp	130		135		140	
Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp	145		150		155	
Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly	165		170		175	
Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser	180		185		190	
Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val	195		200		205	
Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly	210		215		220	
Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala	225		230		235	
Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln	245		250		255	
Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu	260		265		270	
Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro	275		280			

<210> 25
 <211> 836
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (164)..(463)

<400> 25
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 gcgcccggcc ccgactccgg ggtaaagagc cccggagcgg agcagcgctg gccgcgtgcc 120
 gcctccggag ccggcagccc ccatggctgg gggttatgga gtg atg ggt gac gat 175

Met Gly Asp Asp
1

ggt tct att gat tat act gtt cac gaa gcc tgg aat gaa gcc acc aat 223
Gly Ser Ile Asp Tyr Thr Val His Glu Ala Trp Asn Glu Ala Thr Asn
5 10 15 20

gtt tac ttg ata gtt atc ctt gtt agc ttc ggt ctc ttc atg tat gcc 271
Val Tyr Leu Ile Val Ile Leu Val Ser Phe Gly Leu Phe Met Tyr Ala
25 30 35

aaa agg aac aaa agg aga att atg agg ata ttc agt gtg cca cct aca 319
Lys Arg Asn Lys Arg Arg Ile Met Arg Ile Phe Ser Val Pro Pro Thr
40 45 50

gag gaa act ttg tca gag ccc aac ttt tat gac acg ata agc aag att 367
Glu Glu Thr Leu Ser Glu Pro Asn Phe Tyr Asp Thr Ile Ser Lys Ile
55 60 65

cgt tta aga caa caa ctg gaa atg tat tcc att tca aga aag tac gac 415
Arg Leu Arg Gln Gln Leu Glu Met Tyr Ser Ile Ser Arg Lys Tyr Asp
70 75 80

tat cag cag cca caa aac caa gct gac agt gtg caa ctc tca ttg gaa 463
Tyr Gln Gln Pro Gln Asn Gln Ala Asp Ser Val Gln Leu Ser Leu Glu
85 90 95 100

tgaaacctca gaaaaagagc aacagaagta attgtttcaa gctcctgatt ctttctacta 523

aatcatgaac agctttaaaa acatttctgt ctgcataaaa ttattttact tgtaactttt 583

ccccattgt tctgtgcatt gttttgcctt tttaaattac atctccaagt ggctcaaaag 643

gccttgacac aggggaacctg cacatatcca ggatatgtgt aaccagcgat ggtgacttga 703

ccttgccaag acctgtgatt ccttcaggat acaatcagt agaaataaaa acacatcttg 763

ggaagtggga atcctggagt ttatgccatt tgcaatatta aaaaataaaa atgcaagtta 823

ttatttcaat aat 836

<210> 26

<211> 100

<212> PRT

<213> Homo sapiens

<400> 26

Met Gly Asp Asp Gly Ser Ile Asp Tyr Thr Val His Glu Ala Trp Asn
1 5 10 15

Glu Ala Thr Asn Val Tyr Leu Ile Val Ile Leu Val Ser Phe Gly Leu
20 25 30

Phe Met Tyr Ala Lys Arg Asn Lys Arg Arg Ile Met Arg Ile Phe Ser
35 40 45

Val Pro Pro Thr Glu Glu Thr Leu Ser Glu Pro Asn Phe Tyr Asp Thr
50 55 60

Ile Ser Lys Ile Arg Leu Arg Gln Gln Leu Glu Met Tyr Ser Ile Ser
65 70 75 80

Arg Lys Tyr Asp Tyr Gln Gln Pro Gln Asn Gln Ala Asp Ser Val Gln
85 90 95

Leu Ser Leu Glu
100

<210> 27
<211> 1022
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (56)..(730)

<400> 27
agccctcccg ccgcccgcgc gcaggtcccg aggagcgcag actgtgtccc tgaca atg 58
Met
1

gga aca gcc gac agt gat gag atg gcc ccg gag gcc cca cag cac acc 106
Gly Thr Ala Asp Ser Asp Glu Met Ala Pro Glu Ala Pro Gln His Thr
5 10 15

cac atc gat gtg cac atc cac cag gag tct gcc ctg gcc aag ctc ctg 154
His Ile Asp Val His Ile His Gln Glu Ser Ala Leu Ala Lys Leu Leu
20 25 30

ctc acc tgc tgc tct gcg ctg cgg ccc cgg gcc acc cag gcc agg ggc 202
Leu Thr Cys Cys Ser Ala Leu Arg Pro Arg Ala Thr Gln Ala Arg Gly
35 40 45

agc agc cgg ctg ctg gtg gcc tcg tgg gtg atg cag atc gtg ctg ggg 250
Ser Ser Arg Leu Leu Val Ala Ser Trp Val Met Gln Ile Val Leu Gly
50 55 60 65

atc ttg agt gca gtc cta gga gga ttt ttc tac atc cgc gac tac acc 298
Ile Leu Ser Ala Val Leu Gly Gly Phe Phe Tyr Ile Arg Asp Tyr Thr
70 75 80

ctc ctc gtc acc tcg gga gct gcc atc tgg aca ggg gct gtg gct gtg 346
Leu Leu Val Thr Ser Gly Ala Ala Ile Trp Thr Gly Ala Val Ala Val
85 90 95

ctg gct gga gct gct gcc ttc att tac gag aaa cgg ggt ggt aca tac 394
Leu Ala Gly Ala Ala Ala Phe Ile Tyr Glu Lys Arg Gly Gly Thr Tyr
100 105 110

tgg gcc ctg ctg agg act ctg cta gcg ctg gca gct ttc tcc aca gcc 442
Trp Ala Leu Leu Arg Thr Leu Leu Ala Leu Ala Ala Phe Ser Thr Ala

115	120	125	
atc gct gcc ctc aaa ctt tgg aat gaa gat ttc cga tat ggc tac tct			490
Ile Ala Ala Leu Lys Leu Trp Asn Glu Asp Phe Arg Tyr Gly Tyr Ser			
130	135	140 145	
tat tac aac agt gcc tgc cgc atc tcc agc tcg agt gac tgg aac act			538
Tyr Tyr Asn Ser Ala Cys Arg Ile Ser Ser Ser Ser Asp Trp Asn Thr			
150	155	160	
cca gcc ccc act cag agt cca gaa gaa gtc aga agg cta cac cta tgt			586
Pro Ala Pro Thr Gln Ser Pro Glu Glu Val Arg Arg Leu His Leu Cys			
165	170	175	
acc tcc ttc atg gac atg ctg aag gcc ttg ttc aga acc ctt cag gcc			634
Thr Ser Phe Met Asp Met Leu Lys Ala Leu Phe Arg Thr Leu Gln Ala			
180	185	190	
atg ctc ttg ggt gtc tgg att ctg ctg ctt ctg gca tct ctg gcc cct			682
Met Leu Leu Gly Val Trp Ile Leu Leu Leu Leu Ala Ser Leu Ala Pro			
195	200	205	
ctg tgg ctg tac tgc tgg aga atg ttc cca acc aaa ggg gtg agt ccc			730
Leu Trp Leu Tyr Cys Trp Arg Met Phe Pro Thr Lys Gly Val Ser Pro			
210	215	220 225	
taagaaaaga gaccagaagg aaatgttggga agtgagtggga atctagccat gcctctcctg			790
attattagtg cctggtgctt ctgcaccggg cgtcacctgca tctgactgct ggaagaagaa			850
ccagactgag gaaaagaggc tcttcaacag cccagttat cctggcccca tgaccgtggc			910
cacagccctg ctccagcagc acttgcccat tccttacacc ccttcccat cctgctccgc			970
ttcatgtccc ctctgagta gtcattgtgat aataaactct catgttattg tt			1022

<210> 28
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Gly Thr Ala Asp Ser Asp Glu Met Ala Pro Glu Ala Pro Gln His
 1 5 10 15
 Thr His Ile Asp Val His Ile His Gln Glu Ser Ala Leu Ala Lys Leu
 20 25 30
 Leu Leu Thr Cys Cys Ser Ala Leu Arg Pro Arg Ala Thr Gln Ala Arg
 35 40 45
 Gly Ser Ser Arg Leu Leu Val Ala Ser Trp Val Met Gln Ile Val Leu
 50 55 60
 Gly Ile Leu Ser Ala Val Leu Gly Gly Phe Phe Tyr Ile Arg Asp Tyr
 65 70 75 80

Thr Leu Leu Val Thr Ser Gly Ala Ala Ile Trp Thr Gly Ala Val Ala
85 90 95

Val Leu Ala Gly Ala Ala Ala Phe Ile Tyr Glu Lys Arg Gly Gly Thr
100 105 110

Tyr Trp Ala Leu Leu Arg Thr Leu Leu Ala Leu Ala Ala Phe Ser Thr
115 120 125

Ala Ile Ala Ala Leu Lys Leu Trp Asn Glu Asp Phe Arg Tyr Gly Tyr
130 135 140

Ser Tyr Tyr Asn Ser Ala Cys Arg Ile Ser Ser Ser Ser Asp Trp Asn
145 150 155 160

Thr Pro Ala Pro Thr Gln Ser Pro Glu Glu Val Arg Arg Leu His Leu
165 170 175

Cys Thr Ser Phe Met Asp Met Leu Lys Ala Leu Phe Arg Thr Leu Gln
180 185 190

Ala Met Leu Leu Gly Val Trp Ile Leu Leu Leu Leu Ala Ser Leu Ala
195 200 205

Pro Leu Trp Leu Tyr Cys Trp Arg Met Phe Pro Thr Lys Gly Val Ser
210 215 220

Pro
225